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Identification of class-determining residues in G protein-coupled receptors by sequence analysis.

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G protein-coupled receptors (GPCRs) form a large superfamily of receptors that are characterised by a seven transmembrane helical motif. The functions they perform, such as binding ligands and G proteins, are related to the presence of certain amino acids in critical positions. We have developed a computational sequence pattern correlation technique for the recognition of such function-determining residues. The method searches for residues that are conserved in one class of proteins with a certain function but are different in other classes. The basic idea is that such residues are probably involved in this particular function. This technique was used to find residues that play a role in the binding of endogenous as well as exogenous ligands to various receptors. Many of the residues that were detected have been experimentally determined as important for ligand binding. More importantly, however, we also detected residues that are interesting targets for future mutation studies aimed at elucidating the sequence-function relationship in GPCRs. The information obtained may help improve three-dimensional GPCR models and can be useful for the study of receptor-ligand interactions.

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